

1/8

10 30 50
AAAGCACAGAGACTTCAGGTCTCCAAGGAGATGGGTGGCTGCAGCACAAGAGGCAAGCGGC
M G G C S T R G K R P

70 90 110
CGTCAGCCCTCAGTCTGCTGCTGCTGCTGCTCTCGGGGATGCCAGCCTCTGCCCTCC
S A L S L L L L L L S G I A A S A L P
↑
130 150 170
CCCTGGAGAGCGGTCCCACCGGCCAGGACAGTGTGCAGGATGCCACAGGGGGAGGAGGA
L E S G P T G Q D S V Q D A T G G R R T

190 210 230
CCGGCCTTCTGACTTTCTGCCTGGTGGCATGAGTGGCTTCCCAAGACAGCTCCAGCA
G L L T F L A W W H E W A S Q D S S S T

250 270 290
CCGCTTCAAGGGGTACCCGGAGCTGCTAAGGGCAGGAAAGACCACCCCTCCAGC
A F E G G T P E L S K R | Q E R P P L Q Q

310 330 350
AGCCCCAACACCGGGATAAAAAGCCCTGCAAGAACTTCTTCTGGAAAACCTTCTCCCTCGT
P P H R D | K K | P C K N F F W K T F S S C

370 390 410
GCAAGTAGCCCGAGCCTGACCGGAGCCTGACCGGCCACCTGTGAATGCAGCCGTGGCCT
K

430
GAATAAAGAGTGTCAGT

FIGURE 1

CST 10 RPSALSLLLLLGLIAASALPLESGPTGQDSVQDATGRRRTGLLTFLAW 59
... . | : | : | : | . : . | : . . . :
SST 7 QCALAALCIVLAIGGVTGAPS DPLRQFLQKSLAAATGKQELAKYFLAEL 56
↓ ↓
CST 60 WHEWASQDSSSTAEGGTPELSKRQERPPPLQQ.....PPHRDKKPCK 101
: | . : . . . | : : | . | . . . : | : | . |
SST 57 LSEPNQTENDALEPEDLPQAAEQDEMRLLELQRSANSNPAMAPRERKAGCK 106
↑ ↑
CST 102 NFWKTFSCK
| | | | | | | |
SST 107 NFWKTFTSC

FIGURE 2

GCACCGAGGCT CAGCACGTCC GAGG ATG ATG GGT GGC CGA GGC ACA CGA GGC Met Met Gly Gly Arg Gly Thr Gly Gly	51
1 . 5	
AAG TGG CCC TCA GCC TTC GGG <u>CTG CTG CTG</u> CTC TGG GGG GTC GCA GCC Lys Trp Pro Ser Ala Phe Gly Leu Leu Leu Trp Gly Val Ala Ala	99
10 15 20 25 ↑	
TCC CCC CTT CCC CTG GAG AGT GGC CCT ACT GGC CAG GAC AGT GTG CAG Ser Ala Leu Pro Leu Glu Ser Gly Pro Thr Gly Gln Asp Ser Val Gln	147
30 35 40	
GAA GCC ACC GAG GGG AGG AGC GGC CTT CTG ACT TTC CTT GGC TGG TGG Glu Ala Thr Glu Gly Arg Ser Gly Leu Leu Thr Phe Leu Ala Trp Trp	195
45 50 55	
CAC GAG TGG CCT TCC CAA GCC AGC TCC AGC ACC CCC CTC GGA GGG GGT His Glu Trp Ala Ser Gln Ala Ser Ser Thr Pro Val Gly Gly	243
60 65 70	
ACC CCC GGG CTG TCC AAG AGC <u>CAG GAA AGG CCA CCC CCC CAA CAG CCC</u> Thr Pro Gly Leu Ser Lys Ser Gln Glu Arg Pro Pro Pro Gln Gln Pro	291
75 80 85	
<u>CCA CAC CTG GAT AAA AAG CCC TGC AAG AAC TTC TTC TGG AAA ACC TTC</u> <u>Pro His Leu Asp Lys Lys Pro Cys Lys Asn Phe Phe Trp Lys Thr Phe</u>	339
90 95 100 105	
TCC TCG TGC AAG TAA CCC CAC CCT GGG CAT AGC ACC CTG GCC ACC CTG Ser Ser Cys Lys *	387
110 115 120	
TGA GAT GCC AAC GAG ACC TGA ATA AAG ACT GTC AAT CAA C	427
125 130	

FIGURE 3

MOUSE CST	GCACGAG GCTCAGCACG TCCGAGGATG ATGGGTGGCC		
RAT CST	AAAGCACAG ACTTCAGGTC TCCAAGGAGG ATGGGTGGCT		
HUMAN CST	GGCACGAGGC	CAAACATTGA	TTTCAGGGCT GCCAGG PI GG AAGAGCAGCA		
MOUSE CST	GAGGCACAGG	AGGCAAGTGG	CCCTCAG.....	CCTTC
RAT CST	GCAGCACAAAG	AGGCAAGCGG	CCGTCAG.....	CCCTC
HUMAN CST	GCAGGGTGGG	AGAGAAGCTC	CAGTCAGCCC ACAAGATGCC ATTGTCCCCC		
MOUSE CST	GG.....	.GCTGCTGCT	GCTCTGGGGG GTCGCAGCCT CCGCCCTTCC		
RAT CST	<u>AGTCTGCTGC</u>	<u>GGCTGCTGCT</u>	<u>GCTCTGGGGG ATCGCAGCCT CTGCCCTCCC</u>		
HUMAN CST	<u>GGCCTCCTGC</u>	<u>GGCTGCTGCT</u>	<u>CTCCGGGGCC ACGGCCACCG CTGCCCTGCC</u>		
MOUSE CST	CCTGGAGAGT	GGCCCTACTG	GCCAGGACAG	TGTG	CAGGAAGCCA
RAT CST	CCTGGAGAGC	GGTCCCACCG	GCCAGGACAG	TGTG	CAGGATGCCA
HUMAN CST	CCTGGAGGGT	GGCCCCACCG	GCCGAGACAG CGAGCATATG CAGGAAGCGG		
MOUSE CST	C...CGAGGG	GAGGAGCGGC	CTTCTGACTT TCCTTGCTG GTGGCACGAG		
RAT CST	CAGGCGGGAG	GAGGACCGGC	CTTCTGACTT TCCTTGCTG GTGGCATGAG		
HUMAN CST	CAGGAATAAG	AAAAAGCAGC	CTCCTGACTT TCCTCGCTG GTGGTTTGAG		
MOUSE CST	TGGGCTTCCC	AAGCCAGCTC	CAGCACCCCC GTCGGAGGGG GTACCCCCGG		
RAT CST	TGGGCTTCCC	AAGACAGCTC	CAGCACCGCT TTCGA AG GGGG GTACCCCCGGA		
HUMAN CST	TGGACCTCCC	AGGCCAGTG	CGGGCCCCTC ATAGGA AG GGG AAGCCCCGGGA		
MOUSE CST	GCTGTCCAAG	AGCCAGGAAA	GGCCACCCCC CCAACAGCCC CCACACCTGG		
RAT CST	GCTGTCTAAG	CGGCAGGAAA	GACCACCCCT CCAGCA AG CCC CCACACCGGG		
HUMAN CST	GGTGGCCAGG	CGGCAGGAAG	GCGCACCCCC CCAGCA AT CC GCGGCCGGG		
MOUSE CST	ATAAAAAGCC	CTGCAAGAAC	TTCTTCTGGA AAACCTTCTC CTCGTGCAAG		
RAT CST	ATAAAAAGCC	CTGCAAGAAC	TTCTTCTGGA AAACCTTCTC CTCGTGCAAG		
HUMAN CST	ACAGAATGCC	CTGCAGGAAC	TTCTTCTGGA AGACCTTCTC CTCCTGCAAA		
MOUSE CST	TAACCCCACC	CTGGGCATAG	CACCCGGCC ACCCTGTGAG ATGCCAACGAG		
RAT CST	TAGCCCGAGC	CTGACCGGAG	CCTGACCGGC CACCCGTGGA ATGCAGCCGT		
HUMAN CST	TAAAACCTCA	CCCATGAATG	C..... TCACGCAAG TGTAATGACA		
MOUSE CST	GACCTGAATA	AAGACTGTCA	ATCAAC.....		
RAT CST	GGCCTGAATA	AAGAGTGTCA	AGT.....		
HUMAN CST	GACCTGAATA	AAATGTATT	AGCAGCAGTG ATCTTTCCTC TCCTCCTTCC		
MOUSE CST		
RAT CST	CAAGTCATTG	AAAAGTGT	TTTAAATTAAT TTCCATAATA GCCCAATACT		
HUMAN CST		
MOUSE CST		
RAT CST	GACGTGTCTT	GAGTAATTG	GAACCCAAAA GTGAAGATCT TTGATAAAAGA		
HUMAN CST		
MOUSE CST		
RAT CST	TTTTTTTGT	GGTTCGACTG	GAATGTGCTG AGTGC GG CA CTGGGCTTT		
HUMAN CST		
MOUSE CST		
RAT CST	CTTCTGATGT	TCATTATGGT	GCTGGGAAGC TCTGTCTTG ATTTAAAATA		
HUMAN CST		
MOUSE CST		
RAT CST	AAATAGCTAA	AGGCTACAC		
HUMAN CST		

FIGURE 3a

	1	50
RAT CST	.MGGCSTRGK RPSALSLLL LLLSGIAASA LP LESGPTGQ DS..VQDATG	
MOUSE CST	MMGGRG TGK WPSAFGLLLL W...GVAASA LP LESGPTGQ DS..VQEATE	
HUMAN CST MPLSPGLLLL LL SGATATAA LP LEGGPTGR DSEHMQEAAAG	
Consensus	----- -P---LLL -----A--A LP LE-GPTG- DS---Q-A--	
	51	100
RAT CST	GRRTGLLTFL AWWHEWASQD SS STAFEGGT PELSKRQERP PLQQPPHRDK	
MOUSE CST	G.RSGLLTFL AWWHEWASQA SS STPVGGGT PGLSKSQERP PPQQPPHL DK	
HUMAN CST	IRKSSL LTFL AWWFEWTSQA SAGPLIGEEA REVARRQE GA PPQQSARRDR	
Consensus	-----LLTFL AWW-EW-SQ- S----- -----QE-- P-QQ----D-	
	101 116	
RAT CST	KPCKNFFWKT FSSCK	
MOUSE CST	KPCKNFFWKT FSSCK	
HUMAN CST	MPCRNFFWKT FSSCK	
Consensus	-PC-NFFWKT FSSCK	

FIGURE 3b

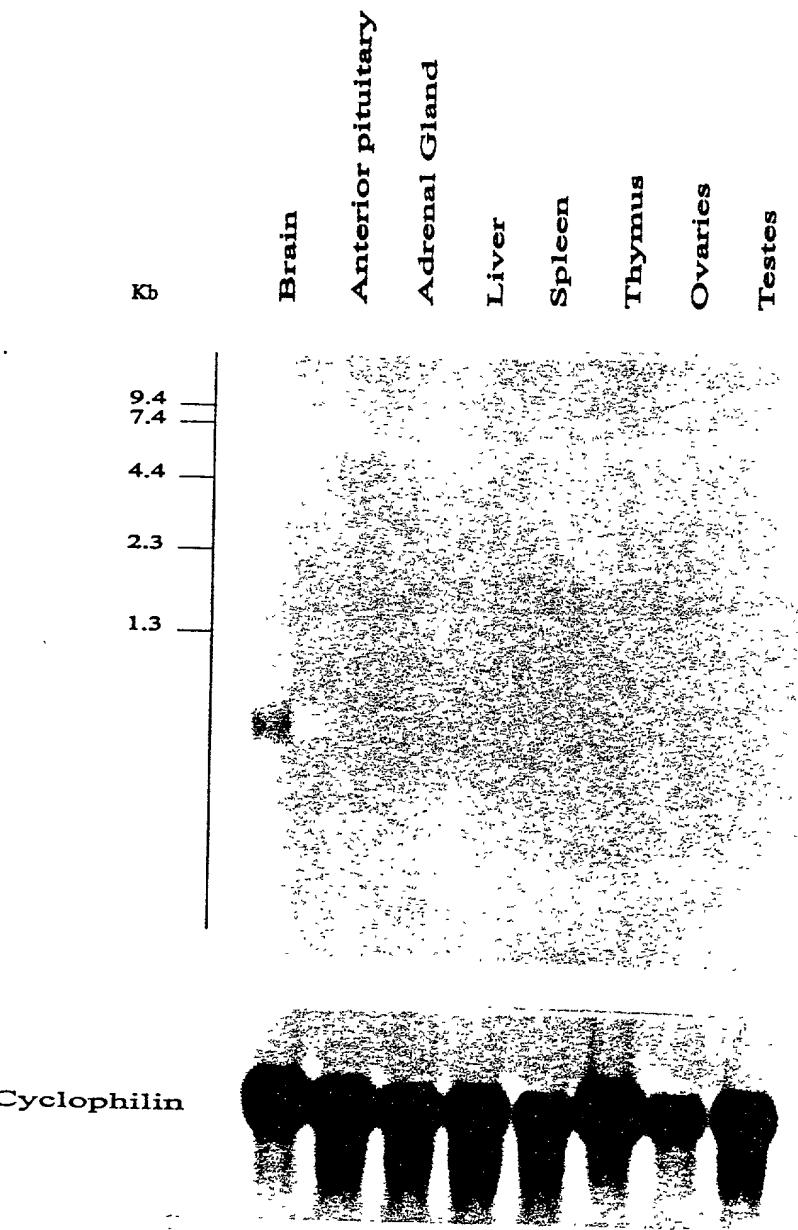
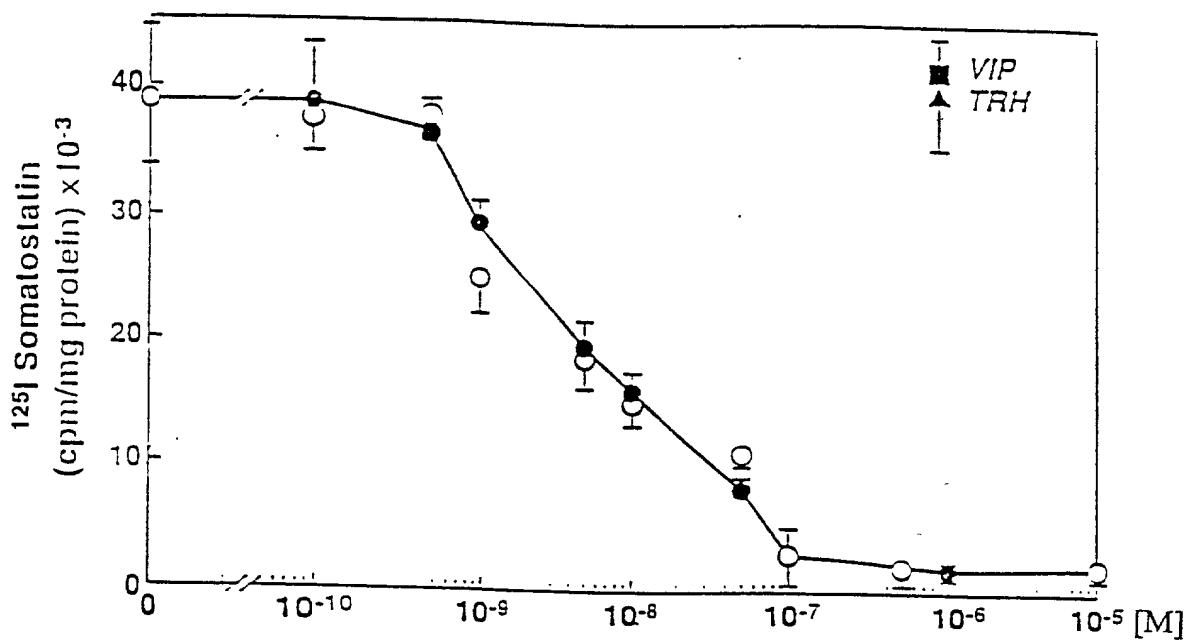
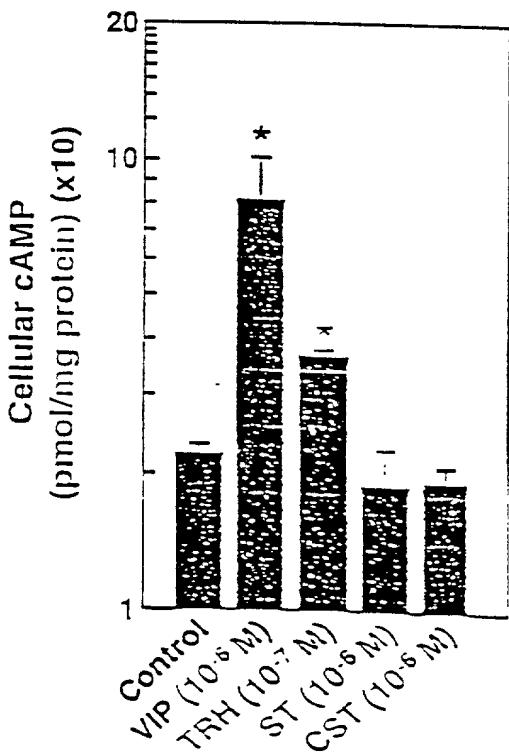


FIGURE 4

5A



5B



5C

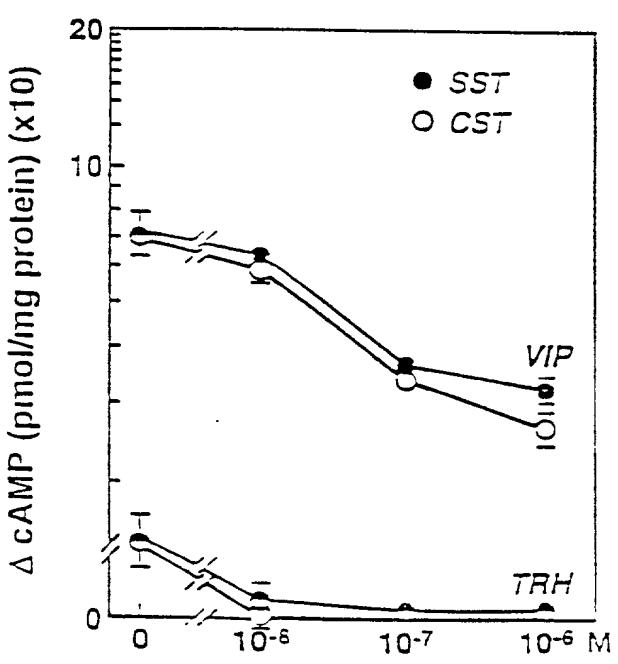
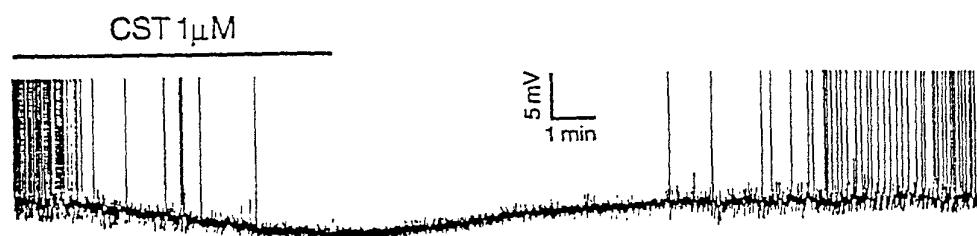
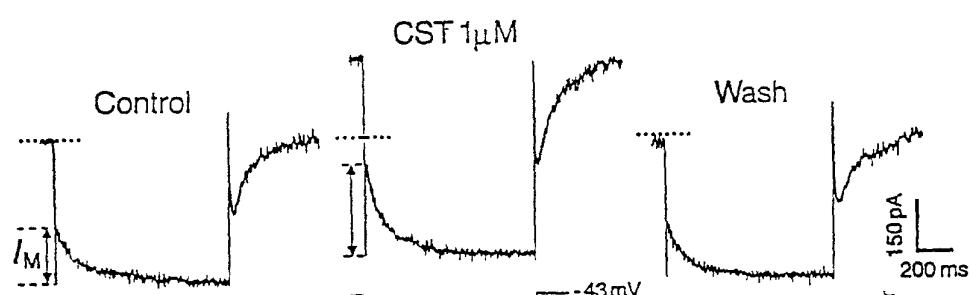


FIGURE 5

6A



6B



6C

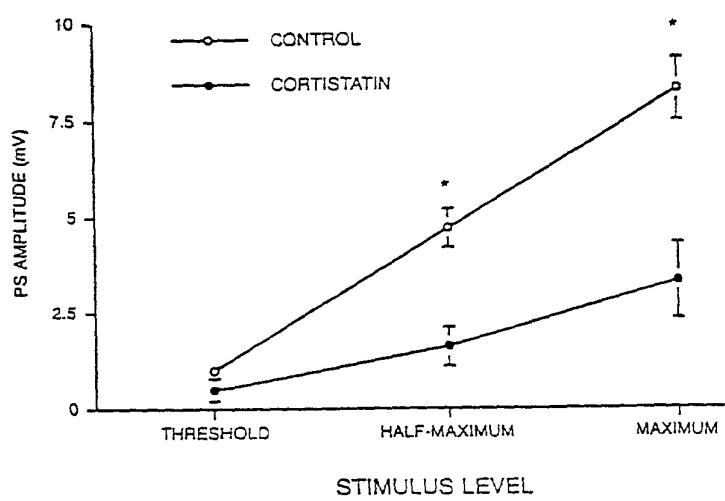
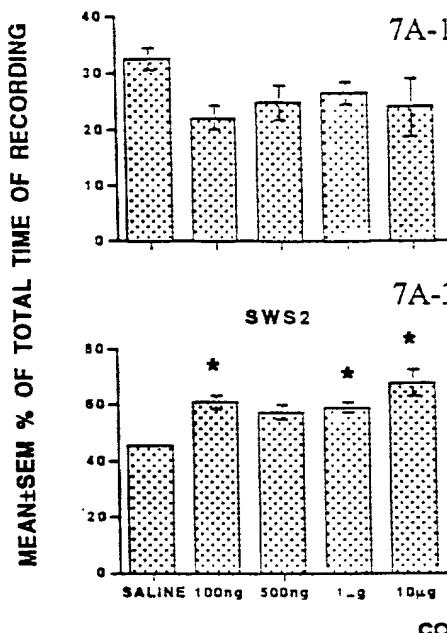


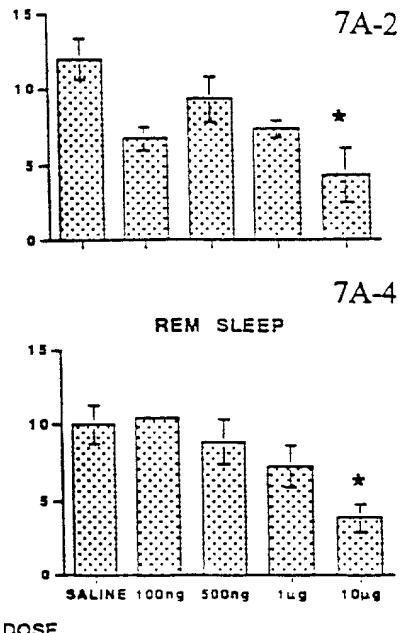
FIGURE 6

7A

WAKEFULNESS

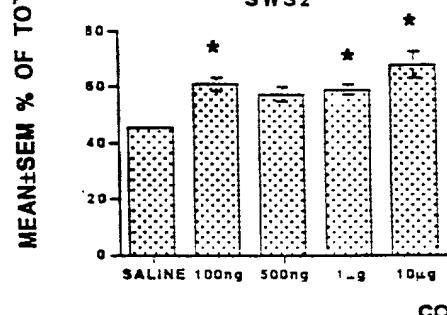


SWS1



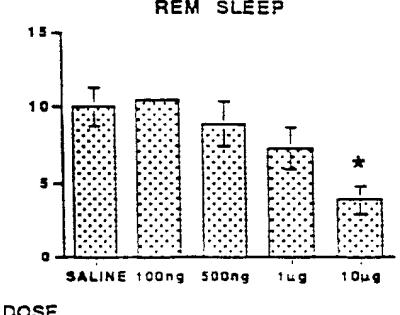
SWS2

7A-3



REM SLEEP

7A-4



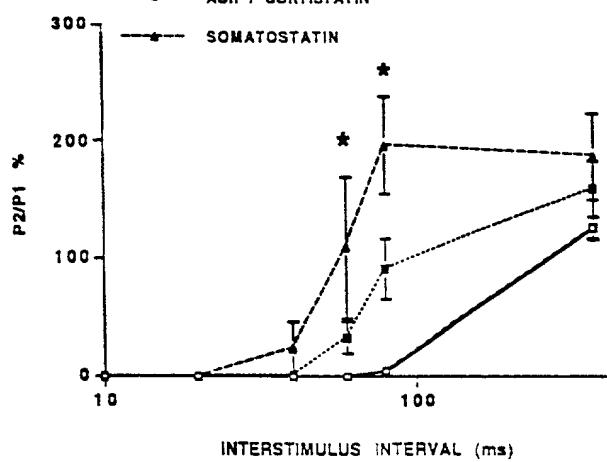
7B

CONTROL

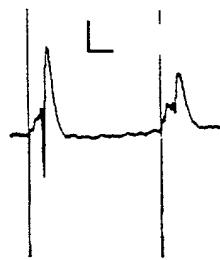
ACh

ACh / CORTISTATIN

SOMATOSTATIN



7C



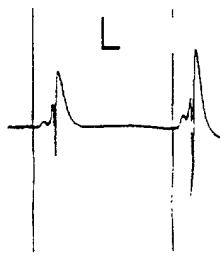
7D



7E



7F



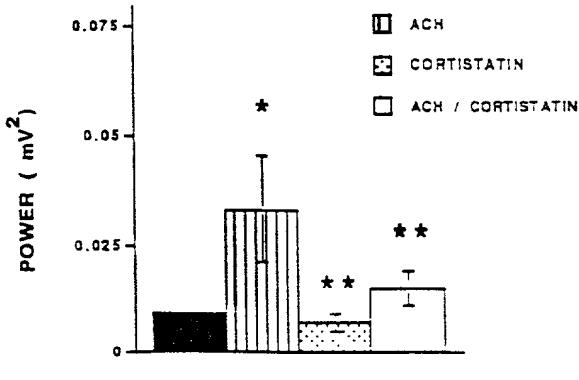
7G

BASELINE

ACh

CORTISTATIN

ACh / CORTISTATIN



FAST ACTIVITY

FIGURE 7